

Dryland Soil Greenhouse Gas Emissions Affected by Cropping Sequence and Nitrogen Fertilization

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Information is needed to mitigate dryland soil greenhouse gas (GHG) emissions by using novel management practices. We evaluated the effects of cropping sequence and N fertilization on dryland soil temperature and water content at the 0- to 15-cm depth and surface CO₂, N₂O, and CH₄ fluxes in a Williams loam (fine-loamy, mixed, superactive, frigid, Typic Argiustolls) in eastern Montana. Treatments were no-tilled continuous malt barley (*Hordeum vulgare* L.) (NTCB), no-tilled malt barley-pea (*Pisum sativum* L.) (NTB-P), and conventional-tilled malt barley-fallow (CTB-F) (control), each with 0 and 80 kg N ha⁻¹. Gas fluxes were measured at 3 to 14 d intervals using static, vented chambers from March to November 2008 to 2011. Soil temperature varied but water content was greater in CTB-F than in other treatments. The GHG fluxes varied with date of sampling, peaking immediately after substantial precipitation (>15 mm) and N fertilization during increased soil temperature. Total CO₂ flux from March to November was greater in NTCB and NTB-P with 80 kg N ha⁻¹ than in other treatments from 2008 to 2010. Total N₂O flux was greater in NTCB with 0 kg N ha⁻¹ and in NTB-P with 80 kg N ha⁻¹ than in other treatments in 2008 and 2011. Total CH₄ uptake was greater with 80 than with 0 kg N ha⁻¹ in NTCB in 2009 and 2011. Because of intermediate level of CO₂ equivalent of GHG emissions and known favorable effect on malt barley yield, NTB-P with 0 kg N ha⁻¹ might mitigate GHG emissions and sustain crop yields compared to other treatments in eastern Montana. For accounting global warming potential of management practices, however, additional information on soil C dynamics and CO₂ associated with production inputs and machinery use are needed.

Abbreviations: CTB-F, conventional-tilled malt barley-fallow; GHG, greenhouse gas; NTB-P, no-tilled malt barley-pea; NTCB, no-tilled continuous malt barley.

Carbon sequestration in soil helps to reduce CO₂ concentration, a major GHG, and mitigates the radiative forcing of the atmosphere in global warming (Lal et al., 1995; Paustian et al., 1995). The process occurs as a result of CO₂ absorption by plants from the atmosphere through photosynthesis which is converted into soil organic matter after the residue is returned to the soil (Lal et al., 1995; Paustian et al., 1995). In contrast, root and microbial respiration and mineralization of soil organic matter and crop residue emit CO₂ from the soil (Curtin et al., 2000; Sainju et al., 2010). Carbon storage in unmanured soil is determined by the balance between the amount of plant residue C added to the soil and rate of C mineralized as CO₂ emissions (Rasmussen et al., 1980; Peterson et al., 1998). Other GHGs emitted from agricultural activities are N₂O and CH₄. Mineralization of crop residue and soil organic matter also emit N₂O and applica-

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tions of manures and N fertilizer augment the process (Mosier et al., 2006; Sey et al., 2008). Nitrous oxide emissions are controlled by nitrification and denitrification processes which are regulated by N substrate availability, available C, and soil temperature, water content, and texture (Drury et al., 2006; Dusenbury et al., 2008). In semiarid regions, aerobic agricultural soils typically act as small sink for atmospheric CH₄ (Bronson and Mosier, 1994).

About 6% of the total GHG emissions in the United States are contributed by agricultural activities (Greenhouse Gas Working Group, 2010; USEPA, 2011). The amount of CO₂ and N₂O emissions contributed by agriculture account for about 25 and 70%, respectively, of the total anthropogenic emissions (Cole et al., 1997; Smith et al., 2007). Fossil fuel consumption, land conversion to cropland, lime application, and N fertilization are major sources of agriculture CO₂ emissions while soil management practices contribute about 92% of the total N₂O emissions (USEPA, 2011). Enteric fermentation and manure management account for 96% of the total CH₄ emissions from agriculture (USEPA, 2011). Although emitted in small amounts, N₂O and CH₄ are considered as potent GHGs because of their greater global warming potential (298 and 25 times, respectively, more powerful than CO₂) (IPCC, 2007).

Although information is available about the use of improved management practices to increase C sequestration in dryland soils (Halvorson et al., 2002; Sainju et al., 2009, 2011), relatively little is known about GHG emissions from agricultural practices. Some of the management practices that affect CO₂, N₂O, and CH₄ emissions in dryland soil are tillage, cropping system, and N fertilization (Curtin et al., 2000; Lemke et al., 1999; Sainju et al., 2010). Reduction in tillage intensity reduces soil disturbance and microbial activity, which in turn, lowers CO₂ and N₂O emissions (Lemke et al., 1999; Drury et al., 2006; Mosier et al., 2006). In contrast, CO₂ emissions increase with increased tillage intensity by improving soil aeration and disrupting soil aggregates (Roberts and Chan, 1990) and by physical degassing of dissolved CO₂ from the soil solution (Jackson et al., 2003). Cropping system can affect the quality and quantity of crop residue returned to the soil and influence CO₂ and N₂O emissions (Mosier et al., 2006; Sainju et al., 2010). Nitrogen fertilization usually stimulates N₂O emissions (Mosier et al., 2006; Dusenbury et al., 2008; Robertson and Vitousek, 2009) but affects variably on CO₂ emissions (Al-Kaisi et al., 2008; Sainju et al., 2010). Nitrogen fertilization also has variable effects on CH₄ emissions (Bronson and Mosier, 1994; Powlson et al., 1997; Amos et al., 2005; Mosier et al., 2006).

Management practices can also indirectly affect CO₂, N₂O, and CH₄ emissions by altering soil temperature and water content, since these parameters are related with GHG emissions (Parkin and Kaspar, 2003; Dusenbury et al., 2008; Liebig et al., 2010). Tillage can dry soil through increased evaporation but no-tillage can conserve soil water and reduce temperature because of decreased disturbance and increased residue accumulation at the surface layer (Curtin et al., 2000; Al-Kaisi and Yin, 2005). Similarly, cropping sequence and crop species can

influence soil temperature and water content by affecting shade intensity and evapotranspiration (Curtin et al., 2000; Amos et al., 2005). Nitrogen fertilization can reduce soil temperature and water content compared to no N fertilization by increasing shade intensity and water uptake through increased biomass production (Sainju et al., 2010).

Limited information is available about the effect of management practices on dryland soil GHG emissions in semiarid regions in the northern Great Plains. We hypothesized that NTB-P with no N fertilization would mitigate dryland soil CO₂, N₂O, and CH₄ emissions compared to NTCB and CTB-F with or without N fertilization. Our objectives were to: (i) quantify the effects of tillage and cropping sequence combination, crop species, and N fertilization on CO₂, N₂O, and CH₄ fluxes under dryland cropping systems from March to November 2008 to 2011, in eastern Montana and (ii) identify a management practice that mitigates GHG fluxes.

MATERIALS AND METHODS

Experimental Site and Treatments

Soil GHG fluxes were measured from 2008 to 2011 in an experiment established in 2006 on a dryland farm, 11 km west of Sidney (48°33' N, 104°50' W), MT. The site is characterized by wide variations in mean monthly air temperature from -8°C in January to 23°C in July and August. The mean annual precipitation (105-yr average) is 350 mm, 80% of which occurs from March to November. The soil is Williams loam with 350 g kg⁻¹ sand, 325 g kg⁻¹ silt, 325 g kg⁻¹ clay, and 7.2 pH at the 0- to 20-cm depth. Soil organic C concentrations at 0- to 5- and 5- to 20-cm depths at the initiation of the experiment in April 2006 were 13.3 and 10.6 g kg⁻¹, respectively. Previous cropping system for the past 6 yr was conventional-tilled spring wheat (*Triticum aestivum* L.)-fallow-safflower (*Carthamus tinctorius* L.).

Main-plot treatments were three 2-yr sequences of NTCB (or malt barley-malt barley), NTB-P, and CTB-F, each with two subplot N fertilization rates of 0 and 80 kg N ha⁻¹. All cropping sequences had two phases (Phase I and Phase II) that occurred every year. Phase I in NTCB, NTB-P, and CTB-F had malt barley, pea, and fallow, respectively, and Phase II had malt barley in all cropping sequences in the first year. In the second year, crops were switched between phases within a sequence, thereby completing rotation of crops in 2 yr. The CTB-F with 80 kg N ha⁻¹ is the control treatment that had been conventionally used by farmers at the site. Malt barley was planted annually in NTCB, in rotation with pea in NTB-P, and in rotation with fallow in CTB-F. The 80 kg N ha⁻¹ is the recommended rate of N fertilization to dryland malt barley at the experimental site. In NTCB and NTB-P, plots were left undisturbed, except for fertilizer application and seeding. In CTB-F, plots were tilled with a field cultivator equipped with C-shanks and 45-cm wide sweeps and coiled-toothed spring harrows with 60-cm rods. Plots were tilled to a depth of 10 cm during planting and fallow periods two to three times a year for seedbed preparation and to control weeds. In the first phase of the cropping sequence, N

fertilizer was applied to malt barley at 80 kg N ha^{-1} but was not applied to pea and fallow. In the second phase, N fertilizer was applied to malt barley at 0 or 80 kg N ha^{-1} in all treatments. Soil $\text{NO}_3\text{-N}$ content to a depth of 60 cm was deducted from N rates before applying N fertilizer. Weeds in no-tilled treatments were controlled by applying preplant and postharvest herbicides and in conventional-tilled treatment by a combination of herbicides and conventional tillage to a depth of 10 cm as needed. Treatments were laid out in split-plot arrangement in a randomized complete block with three replications. The size of the main plot including two phases of the cropping sequence was 24.0 by 12.0 m and split plot was 12.0 by 6.0 m.

Crop Management

In April 2006 to 2011, six-row malt barley (cultivar Certified Tradition [Busch Agricultural Resources, Fargo, ND]) was planted to a depth of 3.8 cm at 45 kg ha^{-1} and pea (cultivar Majoret [Macintosh Seed, Havre, MT]) at 101 kg ha^{-1} with a no-till drill equipped with double-shoot Barton (<http://www.flexicoil.com/barton.asp>) disk openers. Pea seeds were inoculated with proper *Rhizobium* sp. At the same time, N fertilizer as urea (46% N) at 80 kg N ha^{-1} , P fertilizer as triple superphosphate (45% P) at 29 kg P ha^{-1} , and K fertilizer as muriate of potash (60% K) at 27 kg K ha^{-1} were banded to malt barley at 3.8-cm depth, 2.5 cm away from the seed, in the first phase of the cropping sequence. For pea in the first phase and malt barley in the second phase, P and K fertilizers from sources and at rates specified to malt barley as above were banded. In the second phase, N as urea was broadcast at 0 or 80 kg N ha^{-1} to malt barley in all treatments a week after planting. No fertilizers were applied to the fallow phase. No irrigation was applied. In August 2006 to 2011, malt barley and pea grain yields were determined from a swath of 12.0 by 1.5 m using a combine harvester and biomass (stems + leaves) yields from two 0.5 m^2 areas outside yield rows. Both grain and biomass yields were determined on oven-dried basis after drying samples at 60°C for 3 d. After grain harvest, crop biomass residues were returned to the soil.

Greenhouse Gas Measurements

Soil surface CO_2 , N_2O , and CH_4 fluxes were measured from 0900 to 1200 h in the same day at 3- to 14-d intervals, depending on crop growth, from March to November 2008 to 2011, using a static, vented chamber (Hutchinson and Mosier, 1981). Measurements were made at 3-d intervals during the first 2 mo after planting to measure CO_2 flux due to root and microbial respiration during active crop growth, N_2O flux due to N fertilization, and GHG fluxes due to major precipitation events. As the rate of crop growth and precipitation events declined and the effect of N fertilizer on N_2O flux diminished due to N uptake by crop, measurements were made at 7-d intervals thereafter until crop harvest. Since little GHG emissions occur after crop harvest in the fall due to reduced soil temperature and water content (Dusenbury et al., 2008; Liebig et al., 2010), measurements were made at 14-d intervals during this period. The chamber

contained an anchor and a cover as two-piece system which were made of polyvinyl chloride (20 cm i.d.). The anchor (15 cm tall) was inserted into the soil at a nearly leveled surface to a depth of 7.5 cm by hand in each treatment. A carpenter's level was used at the top to level the anchor in the north-south and east-west directions. The cover (10 cm tall), with ports for ventilation and gas collection, was placed at the top of anchor during sampling. At sampling, a rubber sheet attached to the cover was lowered to seal the anchor so that no exchange of gas takes place between the inside and the outside of the chamber. Total headspace volume of the chamber was determined by adding inside volumes of the anchor above the soil surface and the cover. Chambers were removed during tillage, planting, and fertilization operations and reinstalled near the initial location covering crop row and inter-row, with adjusted similar headspace volume as above. Because installation of multiple chambers per plot hindered field operations and soil C and N levels were nearly homogeneous at the site, it was decided to install only one chamber per split plot (or four chambers per main plot). Gas samples were collected after 24 h of anchor installation to stabilize the chamber in the soil. Gas samples were collected at 0, 20, and 40 min by injecting a needle attached to a 20-mL syringe in the sampling port and transferring in 12-mL evacuated glass vials sealed with butyl rubber septa (Labco Ltd., High Wycombe, UK). Plants that grew above the height and circumference of the chamber were either squeezed inside or trimmed before the measurement of gas fluxes when needed to reduce the error associated with connecting the top and bottom portions of the chamber. Since excessive growth of crop biomass was trimmed regularly to fit plants inside the chamber, no attempt was made to measure the amount of biomass trimmed or inside the chamber. Concentrations of CO_2 , N_2O , and CH_4 in gas samples inside vials were determined with a gas chromatograph (Model 3800, Varian, Palo Alto, CA) in the laboratory within a week of collection. The gas chromatograph was fully automated with thermoconductivity, flame ionization, and electron capture detectors for analysis of CO_2 , N_2O , and CH_4 concentrations, respectively, in one gas sample. Gas flux was calculated as changes in either linear or curvilinear concentration gradient over time (Hutchinson and Mosier, 1981; Liebig et al., 2010). Total fluxes during the measurement period from March to November in each year were calculated by linearly interpolating data points and integrating the underlying area (Gilbert, 1987). At the time of gas sampling, soil temperature at the 0- to 15-cm depth was measured with a temperature probe and soil water content was determined gravimetrically by collecting field-moist soil sample at 0 to 15 cm with a hand probe (2 cm i.d.) near the chamber and oven drying at 105°C . Because soils were frozen to more than 1-m depth and insignificant fluxes generally occur from December to February, except N_2O flux (Liebig et al., 2010), GHG fluxes and soil temperature and water content were not measured during this period. Since gas chromatograph was available only from July 2008, GHG fluxes were measured from July to November in 2008 instead of March to November in other years.

Data Analysis

Data for GHG fluxes and soil temperature and water content were analyzed using the Analysis of Repeated Measures procedure in the MIXED model of SAS (Littell et al., 1996). Cropping sequence was considered as the main plot and the fixed effect, N fertilization as the split plot and another fixed effect, and date of sampling as the repeated measure variable for data analysis. For analysis of total gas flux or average soil temperature and water content from March to November in a year, cropping sequence, N fertilization, and year were considered as fixed effects as above. Random variables were replication and replication \times cropping sequence interaction. In cropping sequence treatments, data were analyzed separately by phases to evaluate the effect of crop species and averaged across phases to evaluate the effect of cropping sequence on GHG fluxes. Means were separated by using the least square means test when treatments and interactions were significant (Littell et al., 1996). Statistical significance was evaluated at $P \leq 0.05$, unless otherwise stated.

RESULTS AND DISCUSSION

Soil Temperature and Water Content

Soil temperature increased from March to September and then declined in all years (Fig. 1). In 2008, soil temperature was not different among cropping sequences. Soil temperature was greater in CTB-F than in other cropping sequences in May, June, and October 2009, April 2010, and June 2011 but was greater in NTB-P and NTCB in July and August 2010 and August 2011. Averaged across measurement dates, soil temperature was greater in NTCB with 80 kg N ha⁻¹ or NTB-P with 0 kg N ha⁻¹ than in CTB-F and NTB-P with 80 kg N ha⁻¹ from 2009 to 2011 (Table 1). Averaged across cropping sequences and measurement dates, soil temperature was greater with 0 than with 80 kg N ha⁻¹ from 2009 to 2011. While increased soil exposure due to tillage and fallow likely increased soil temperature in CTB-F, reduced shading due to lower biomass production in the absence of N fertilization may have increased temperature with 0 compared with 80 kg N ha⁻¹, a case similar to that reported by Sainju et al. (2010).

In 2008 when precipitation from July to November was below the average, soil was almost dry, with minimal water content

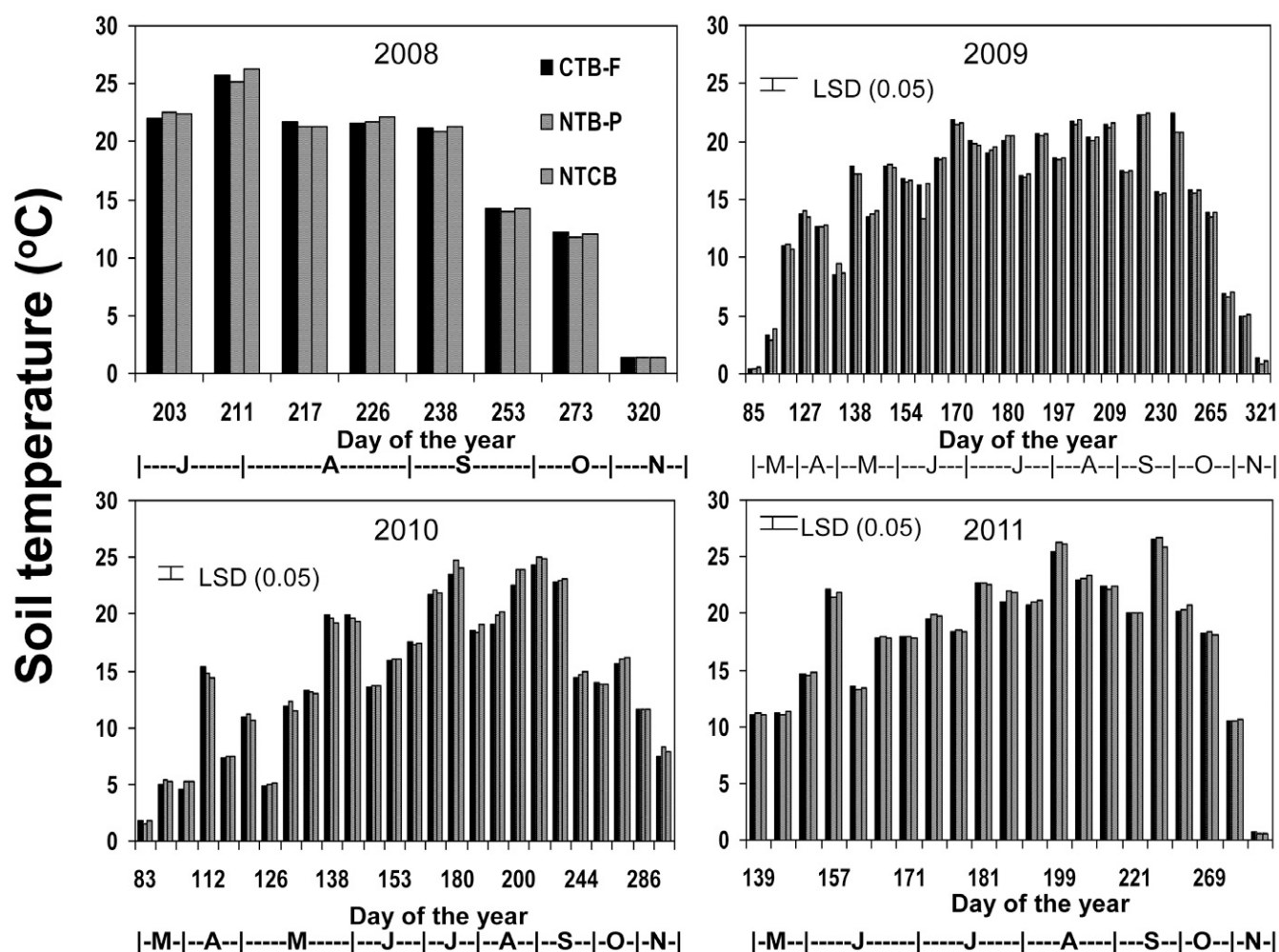


Fig. 1. Effect of cropping sequence on soil temperature at the 0- to 15-cm depth from March to November 2008 to 2011. CTB-F denotes conventional-tilled malt barley-fallow; NTB-P, no-tilled malt barley-pea; and NTCB, no-tilled continuous malt barley. Uppercase letter at the bottom of the figure denotes month of the year.

and no difference among cropping sequences during the measurement period (Fig. 2 and 3). Soil water content, however, responded to precipitation (>15 mm) events during the measurement period from 2009 to 2011, with higher water levels in May and June. Water content was greater in CTB–F than in other cropping sequences in May, July, and August, 2009. Averaged across N fertilization and measurement dates, water content was greater in CTB–F than in NTB–P and NTCB in 2009 (Table 1). Greater water content in CTB–F was likely a result of increased water conservation during fallow due to the absence of plants, a case similar to those observed by various researchers (Lenssen et al., 2007; Liebig et al., 2010; Sainju et al., 2010).

Soil Greenhouse Gas Emissions

Carbon Dioxide

Carbon dioxide flux varied with cropping sequence and date of sampling from 2008 to 2011 and with N fertilization in 2009 and 2010 (Table 2). Interactions were significant for cropping sequence \times N fertilization from 2008 to 2010, cropping sequence \times date of sampling from 2008 to 2011, and N fertilization \times date of sampling in 2009 and 2010. For cropping phases (Phases I and II), CO₂ flux was also significant for cropping sequence, N fertilization, date of sampling, and their interactions from 2008 to 2011.

Carbon dioxide flux peaked following substantial precipitation (>15 mm) events from May to August during increased soil temperature and water content (Fig. 1–6). The flux ranged from 1 kg C ha⁻¹ d⁻¹ in March 2010 to 23 kg C ha⁻¹ d⁻¹ in August 2011 (Fig. 4–6). The high value of CO₂ flux in this experiment was lower than peak values of 80 to 160 kg C ha⁻¹ d⁻¹ under spring wheat in western Canada (Curtin et al., 2000) and 57 kg C ha⁻¹ d⁻¹ under malt barley in eastern Montana (Sainju et al., 2010), both measured by the dynamic chamber method, but >16 kg C ha⁻¹ d⁻¹ under fallow in North Dakota measured by the static chamber method (Liebig et al., 2010). Differences in soil and environmental conditions and management practices among locations and measurement methods can influence CO₂ emissions (Sainju et al., 2012). Most of the CO₂ flux occurred from May to August (>80%), regardless of treatments and years. This is the period when crops actively grow and roots respire, since 30 to 50% of the total CO₂ flux is accounted by root respiration (Rochette et al., 1999; Curtin et al., 2000). Also higher soil temperature and water content due to increased precipitation during this period (Fig. 1–3) likely increased soil microbial activity and C mineralization, thereby resulting in greater CO₂ flux (Van Gestel et al., 1993; Curtin et al., 2000).

Carbon dioxide flux was greater in NTCB and NTB–P than in CTB–F in August and September 2008, from June to

Table 1. Effects of cropping sequence and N fertilization on average soil temperature and water content at the 0- to 15-cm depth across measurement dates from March to November 2008 to 2011.

Cropping sequence†	N fertilization	Soil temperature				Soil water content			
		2008	2009	2010	2011	2008	2009	2010	2011
	kg N ha ⁻¹	°C				g kg ⁻¹			
CTB–F	0	17.78	15.16	14.67	18.15	10.6	116.4	146.9	141.7
	80	17.50	14.91	14.34	17.83	10.4	120.3	146.5	148.4
NTB–P	0	17.46	15.16	15.02	18.26	10.5	102.0	144.5	142.5
	80	17.20	14.85	14.49	17.88	9.7	98.3	144.2	136.0
NTCB	0	17.69	14.94	14.53	18.1	11.2	98.2	137.6	135.5
	80	17.58	15.22	14.79	18.08	10.0	98.2	138.3	136.0
LSD (0.05)		ns‡	0.30	0.31	0.17	ns	ns	ns	ns
Means									
CTB–F		17.49a§	15.04a	14.51a	17.99a	10.5a	118.3a	146.7a	145.0a
NTB–P		17.33a	15.00a	14.75a	18.07a	10.1a	100.2b	144.3a	139.3a
NTCB		17.64a	15.08a	14.66a	18.09a	10.6a	95.2b	138.0a	135.8a
	0	17.54a	15.09a	14.73a	18.17a	10.8a	105.5a	143.0a	139.9a
	80	17.43a	14.99b	14.54b	17.93b	10.0a	105.6a	143.0a	140.2a
Significance									
Cropping sequence (C)		ns	ns	ns	ns	ns	*	ns	ns
N fertilization (F)		ns	*	**	***	ns	ns	ns	ns
C \times F		ns	***	***	**	ns	ns	ns	ns
Date of sampling (D)		***	***	***	***	***	***	***	***
C \times D		ns	*	*	*	ns	**	ns	ns
F \times D		ns	ns	ns	ns	*	ns	ns	ns
C \times F \times D		ns	ns	ns	ns	ns	ns	ns	ns

* Significant at $P = 0.05$.

** Significant at $P = 0.01$.

*** Significant at $P = 0.001$.

† Cropping sequences are CTB–F, conventional-tilled malt barley–fallow; NTB–P, no-tilled malt barley–pea; and NTCB, no-tilled continuous malt barley.

‡ ns, not significant.

§ Numbers followed by different letters in a column within a set are significantly different at $P \leq 0.05$ by the least square means test.

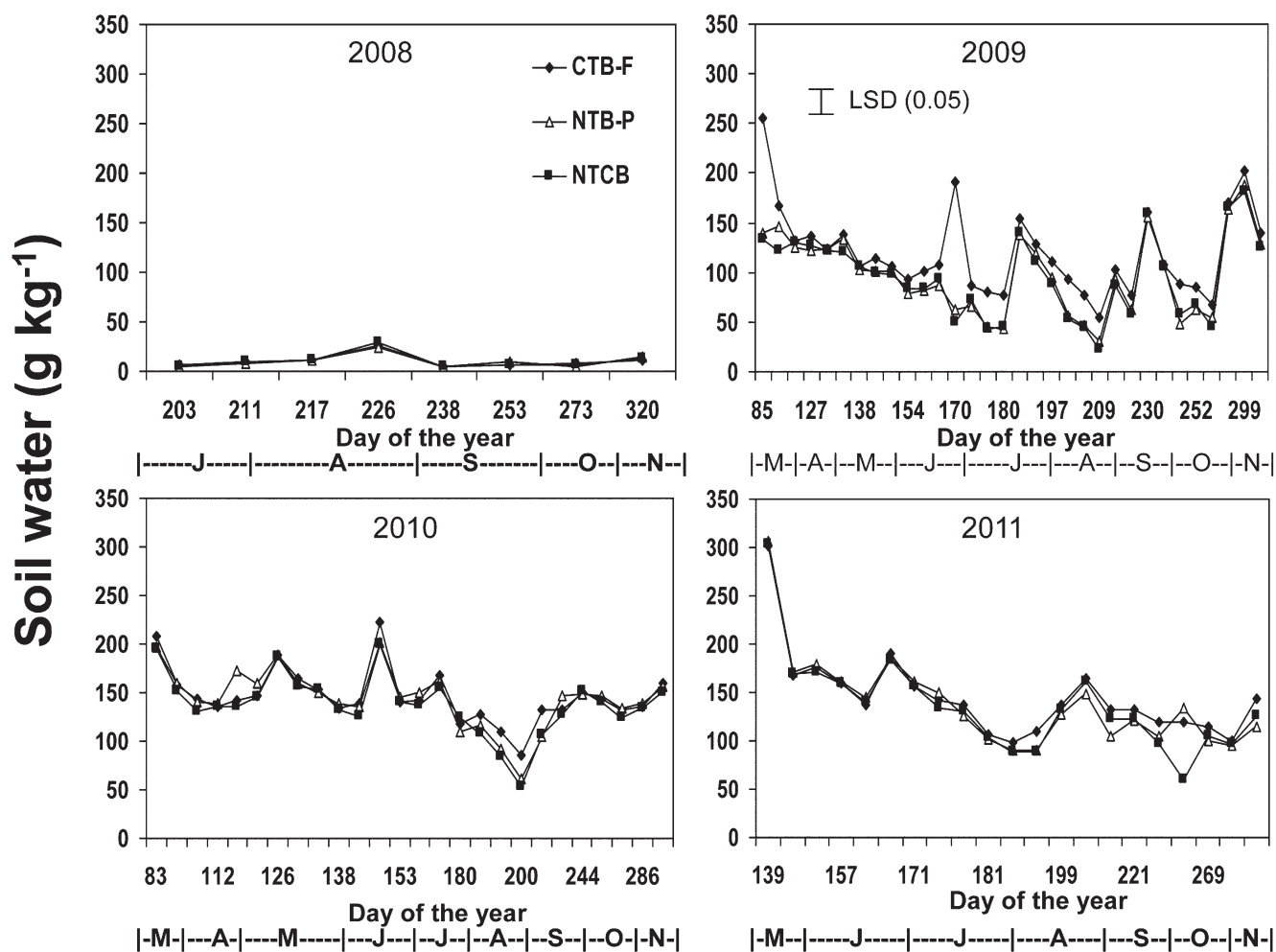


Fig. 2. Effect of cropping sequence on soil water content from at the 0- to 15-cm depth from March to November 2008 to 2011. CTB-F denotes conventional-tilled malt barley-fallow; NTB-P, no-tilled malt barley-pea; and NTCB, no-tilled continuous malt barley. Uppercase letter at the bottom of the figure denotes month of the year.

August 2009, in May, July, and September 2010, and from May to August 2011 (Fig. 4). Decreased root respiration as a result of absence of crops in the fallow year likely reduced CO_2 flux in CTB-F compared to other cropping sequences during these periods, a case similar to that reported by Sainju et al. (2010, 2012). While N fertilization had no effect on CO_2 flux in 2008 and 2011, the flux was greater with 80 than with 0 kg N ha^{-1} in May and June 2009 and in June and July in 2010 (Fig. 5). Total CO_2 flux from March to November was greater in NTCB or NTB-P with 80 kg N ha^{-1} than in CTB-F with 0 or 80 kg N ha^{-1} and in NTB-P with 0 kg N ha^{-1} from 2008 to 2010 (Table 2). Averaged across N fertilization, total CO_2 flux was greater in NTCB than in NTB-P and CTB-F in 2008 and greater in NTCB and NTB-P than in CTB-F from 2009 to 2011. Averaged across cropping sequences, total CO_2 flux was greater with N fertilization than without in 2009 and 2010. Averaged across years, total CO_2 flux was greater in NTCB and NTB-P than in CTB-F and with 80 than with 0 kg N ha^{-1} (Table 3). Averaged across treatments, total CO_2 flux was greater in 2009 than in 2008 and 2010.

In addition to increased root respiration, greater amounts of biomass residue returned to the soil due to continuous cropping and N fertilization probably increased CO_2 flux in NTCB

and NTB-P with N fertilization than in CTBF with or without N fertilization. Sainju et al. (2010) have reported greater amount of annualized biomass (stems and leaves) yield returned to the soil in NTCB and NTB-P (2.42–2.55 Mg ha^{-1}) than in CTB-F (1.45 Mg ha^{-1}) and with 80 (2.96 Mg ha^{-1}) than with 0 kg N ha^{-1} (2.49 Mg ha^{-1}). They have also reported greater total CO_2 flux from May to October in NTCB and NTB-P (2.33–2.48 Mg C ha^{-1}) than in CTB-F (2.18 Mg C ha^{-1}). Probably increased C substrate availability enhanced microbial activity, thereby increasing crop residue mineralization and CO_2 flux in NTCB and NTB-P than in CTB-F. Several researchers (Curtin et al., 2000; Amos et al., 2005) have also reported greater CO_2 flux in cropping systems with increased amount of crop residue returned to the soil. Tillage appeared to have a small effect on CO_2 flux among cropping sequence treatments because of the lower flux in CTB-F. Nitrogen fertilization has been known to have variable effect on CO_2 flux (Mosier et al., 2006; Al-Kaisi et al., 2008; Sainju et al., 2010).

To evaluate the effect of crop species on CO_2 flux, the flux was described by cropping phases (Fig. 6). In Phase I, CO_2 flux was greater under no-tilled malt barley than under no-tilled pea in August and September 2008 and greater under no-tilled malt

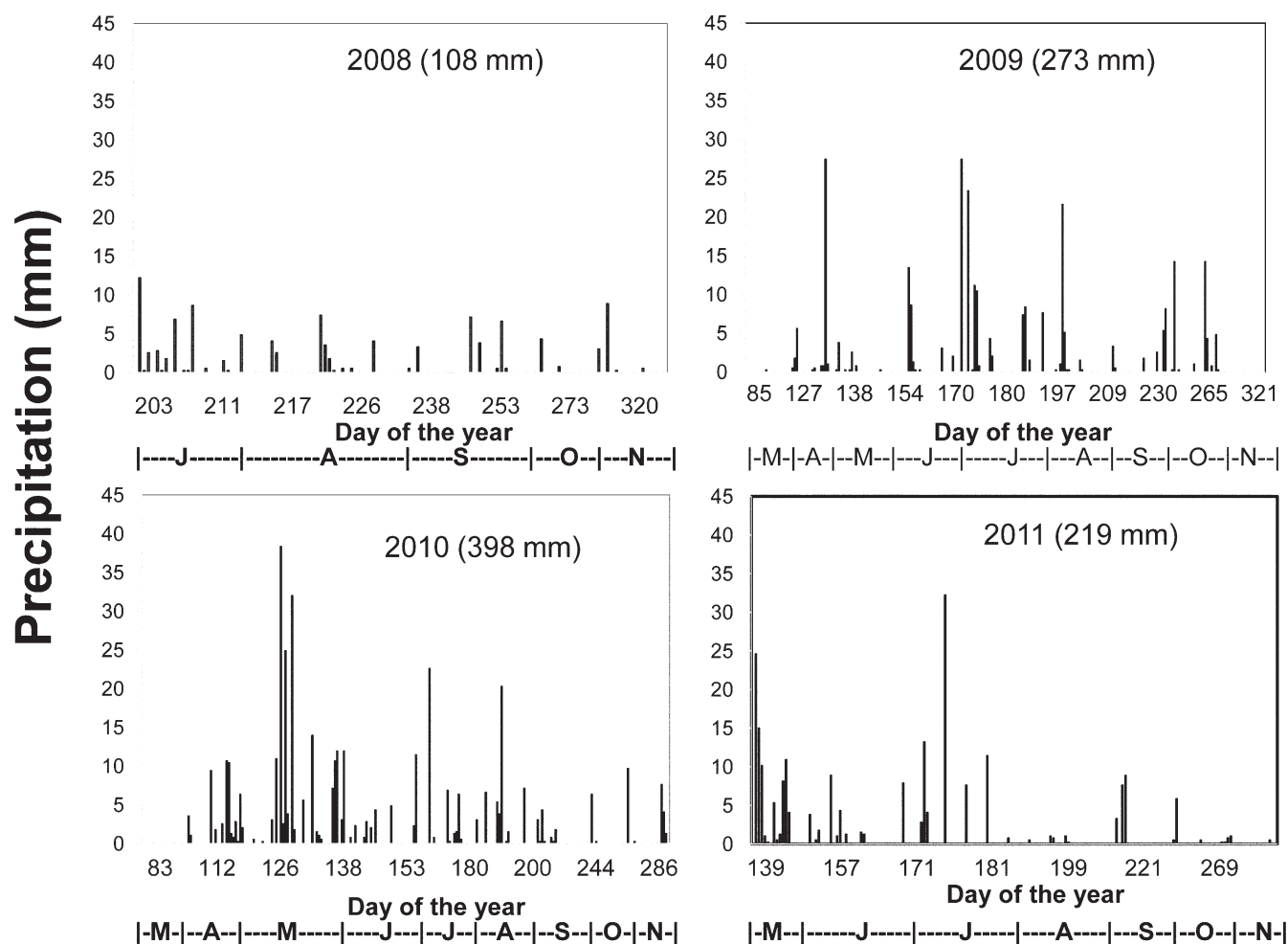


Fig. 3. Daily total precipitation from March to November 2008 to 2011 at the study site. The number in parenthesis denotes total precipitation during the measurement period. Uppercase letter at the bottom of the figure denotes month of the year.

barley and pea than under conventional-tilled fallow from June to August 2009 and 2011 and in June and July 2010. In Phase II, CO₂ flux was greater under malt barley following malt barley in August and September 2008 but was greater under malt barley following fallow in June and July 2010. The CO₂ flux under malt barley following malt barley, pea, and fallow was variable among measurement dates in 2011. Total CO₂ flux from March to November was greater under pea with 80 kg N ha⁻¹ than under other treatments in Phase I, 2009 and 2010 (Table 2). In Phase II, total CO₂ flux was greater under malt barley following malt barley with 80 kg N ha⁻¹ than under other treatments in 2008. Averaged across N fertilization, total CO₂ flux was greater under malt barley than under pea in 2008 and under fallow in 2011 and greater under malt barley and pea than under fallow in 2009 and 2010 in Phase I. Total CO₂ flux under malt barley following malt barley, pea, and fallow were not significantly different among crop species in all years in Phase II. Averaged across cropping sequences, total CO₂ flux was greater with 0 than with 80 kg N ha⁻¹ in 2008 but the trend reversed in 2009 and 2010 in Phase I. In Phase II, total CO₂ flux was greater with N fertilization than without in 2011.

The greater CO₂ flux under no-tilled malt barley and pea than under conventional-tilled fallow was likely the results of in-

creased root respiration due to presence of crops and increased biomass residue returned to the soil, since tillage had little effect on the flux (Sainju et al., 2010). The fact that malt barley increased CO₂ flux compared to pea was probably related to biomass production, since pea produces lower biomass than malt barley and spring wheat (Lenssen et al., 2007; Sainju et al., 2010). Although N fertilizer was not applied to pea, greater CO₂ flux under pea with 80 kg N ha⁻¹ than in other treatments in Phase I was probably the result of pea root respiration and the residual effect of previous years of N fertilization that increased the amount of residue returned to the soil. Similarly, greater CO₂ flux with than without N fertilization in Phase I was probably a result of N fertilization to malt barley. The reasons for greater CO₂ flux with 0 than with 80 kg N ha⁻¹ in 2008 Phase I was not known.

Differences in soil temperature and water content among years probably resulted in various CO₂ flux from 2008 to 2011. Greater CO₂ flux in 2009 than in 2008 and 2010 (Table 3) was probably due to increased soil temperature, precipitation, and soil water content (Table 1, Fig. 3). Increased soil temperature and water content increase microbial activity and C mineralization, thereby resulting in greater CO₂ flux (Parkin and Kaspar, 2003; Amos et al., 2005). Late measurement of GHG emissions probably reduced CO₂ flux in 2008.

Table 2. Effects of cropping sequence and N fertilization on total soil surface CO₂ flux from March to November 2008 to 2011.

Cropping sequence†	N fertilization kg N ha ⁻¹	Total CO ₂ flux‡											
		2008			2009			2010			2011		
		Phase I	Phase II	Mean	Phase I	Phase II	Mean	Phase I	Phase II	Mean	Phase I	Phase II	Mean
		Mg C ha ⁻¹											
CTB-F	0	0.78	0.74	0.76	0.69	1.37	1.03	0.56	1.22	0.89	1.03	1.19	1.11
	80	0.65	0.74	0.70	0.67	1.39	1.03	0.61	1.47	1.04	0.88	1.44	1.16
NTB-P	0	0.68	0.87	0.78	1.24	1.36	1.30	1.09	1.21	1.15	1.28	1.33	1.31
	80	0.62	0.77	0.70	2.19	1.48	1.84	1.54	1.10	1.32	1.26	1.56	1.41
NTCB	0	0.98	0.72	0.85	1.42	1.58	1.50	1.23	1.42	1.33	1.39	1.32	1.36
	80	0.82	1.15	0.99	1.68	1.46	1.57	1.20	1.39	1.30	1.36	1.47	1.42
LSD (0.05)		ns§	0.42	0.15	0.36	ns	0.20	0.32	ns	0.10	ns	ns	ns
Means													
CTB-F		0.72ab¶	0.74a	0.73b	0.68b	1.38a	1.03b	0.58b	1.35a	0.97c	0.96b	1.31a	1.14b
NTB-P		0.65b	0.81a	0.73b	1.71a	1.42a	1.57a	1.31a	1.16a	1.23b	1.27ab	1.44a	1.36a
NTCB		0.90a	0.93a	0.92a	1.56a	1.52a	1.54a	1.22a	1.41a	1.32a	1.37a	1.39a	1.38a
	0	0.82a	0.78a	0.80a	1.12b	1.44a	1.28b	0.96b	1.28a	1.12b	1.23a	1.28b	1.26a
	80	0.70b	0.89a	0.80a	1.52a	1.44a	1.48a	1.12a	1.32a	1.22a	1.17a	1.49a	1.33a
Significance													
Cropping sequence (C)		*	ns	**	**	ns	***	**	ns	***	*	ns	*
N fertilization (F)		*	ns	ns	***	ns	**	*	ns	**	ns	*	ns
C × F		ns	*	*	***	ns	**	*	ns	**	ns	ns	ns
Date of sampling (D)		***	***	***	***	***	***	**	***	***	***	***	***
C × D		*	*	*	***	ns	***	**	***	***	***	*	*
F × D		ns	*	ns	***	ns	*	***	ns	***	ns	ns	ns
C × F × D		ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns

* Significant at $P = 0.05$.

** Significant at $P = 0.01$.

*** Significant at $P = 0.001$.

† Cropping sequences are CTB-F, conventional-tilled malt barley-fallow; NTB-P, no-tilled malt barley-pea; and NTCB, no-tilled continuous malt barley.

‡ Phase I of the cropping sequence includes fallow in CTB-F, pea in NTB-P, and malt barley in NTCB and Phase II includes malt barley in all cropping sequences.

§ ns, not significant.

¶ Numbers followed by different letters in a column within a set are significantly different at $P \leq 0.05$ by the least square means test.

Nitrous Oxide

Nitrous oxide flux varied with cropping sequence in 2011, N fertilization in 2010, and date of sampling from 2008 to 2011 (Table 4). Interactions were significant for cropping sequence × N fertilization in 2008 and 2011 and cropping sequence × date of sampling from 2009 to 2011. Cropping sequence, N fertilization, date of sampling, and their interactions were also significant for N₂O flux for cropping phases in various years.

Nitrous oxide flux increased from 3 g N ha⁻¹ d⁻¹ in July to 9 g N ha⁻¹ d⁻¹ in August and then declined but no difference in the flux among cropping sequences was observed from July to November in 2008 (Fig. 7). In 2009 and 2010, N₂O flux remained at <4 g N ha⁻¹ d⁻¹ and fluxes were greater in CTB-F or NTB-P than in NTCB in July and August. In 2011, a sharp increase in N₂O flux from 2 to 26 g N ha⁻¹ d⁻¹ occurred in May and then declined. Nitrous oxide flux was greater in NTB-P and CTB-F than in NTCB in May and June. The N₂O flux from 0.5 to 26 g N ha⁻¹ d⁻¹ observed in this experiment was within or slightly greater than the range of -8 to 21 g N ha⁻¹ d⁻¹ under spring wheat-pea rotation and fallow in western Montana and central North Dakota (Dusenbury et al., 2008; Liebig et al., 2010). The greater N₂O flux in May and June was likely due to

both N fertilization and increased soil water content from substantial precipitation (>15 mm) and the flux in July and August was probably a result of substantial precipitation and/or increased soil temperature (Fig. 1, 2, 3, and 7). Several researchers (Mosier et al., 2006; Dusenbury et al., 2008; Liebig et al., 2010) have noted increased N₂O flux immediately after N fertilization and/or substantial precipitation. Greater N₂O flux in NTB-P and CTB-F than in NTCB during these periods may have resulted either from increased N contribution from pea residue due to its higher N concentration in NTB-P or increased organic N mineralization due to tillage and/or soil water content during fallow in CTB-F (Table 1). Residues of legumes, such as pea and soybean, in rotation with nonlegumes, such as spring wheat and corn, have been known to produce significant N₂O emissions due to their lower C/N ratio (Mosier et al., 2006; Dusenbury et al., 2008). Similarly, tillage and fallow can increase soil organic N mineralization and NO₃-N content, resulting in greater N₂O emissions (Aulakh et al., 1982; Lemke et al., 1999).

Total N₂O flux from March to November was greater in NTCB with 0 kg N ha⁻¹ or NTB-P with 80 kg N ha⁻¹ than in other treatments in 2008 and 2011 (Table 4). Averaged across N fertilization, total N₂O flux was greater in NTB-P than in

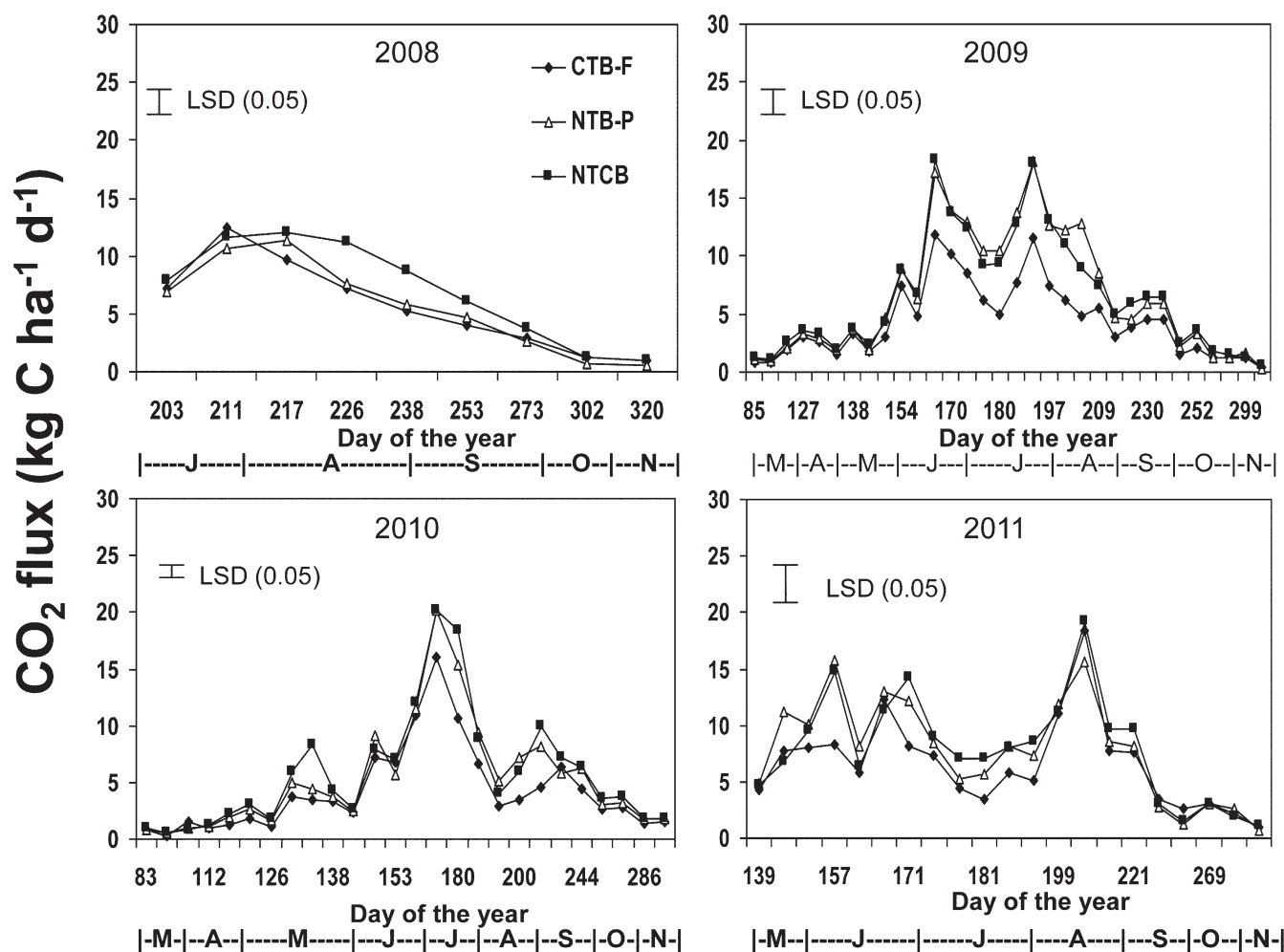


Fig. 4. Effect of cropping sequence on soil surface CO_2 flux from March to November, 2008 to 2011. CTB-F denotes conventional-tilled malt barley-fallow; NTB-P, no-tilled malt barley-pea; and NTCB, no-tilled continuous malt barley. Uppercase letter at the bottom of the figure denotes month of the year.

NTCB in 2011. Averaged across cropping sequences, total N_2O flux was greater with N fertilization than without in 2010. Averaged across years, total N_2O flux was not different among treatments (Table 3). Averaged across treatments, total N_2O flux was greater in 2011 than in other years.

The reasons for greater N_2O flux in NTCB with 0 kg N ha^{-1} were not clear. Greater N_2O flux in NTB-P with 80 kg N ha^{-1} , however, likely resulted from increased N substrate availability from both pea residue and N fertilization. Increased N substrate availability due to N fertilization has been known to increase N_2O flux due to enhanced nitrification (Drury et al., 2006; Mosier et al., 2006; Dusenbury et al., 2008). Although not significant, tillage and fallow appeared to have some effect on N_2O flux, thereby resulting in similar or greater flux in CTB-F than in NTCB. Lemke et al. (1999) found that N_2O emissions was similar or greater in conventional till than in no-till under dry-land cropping systems in Alberta but Robertson et al. (2000) observed greater emissions in no-till than in conventional till in humid regions. The greater N_2O flux in 2011 than in other years was probably due to increased soil temperature (Table 1), since increased temperature can stimulate microbial activity and

N mineralization (Parkin and Kaspar, 2003; Dusenbury et al., 2008; Liebig et al., 2010).

The effect of crop species on N_2O flux can be further revealed by studying fluxes in both phases of the cropping sequence (Fig. 8). In Phase I, N_2O flux was greater under malt barley than under pea and fallow in August 2008 but was greater under fallow than under malt barley and pea in July 2009. In May and June 2011, N_2O flux was greater under pea and fallow than under malt barley. In Phase II, N_2O flux was greater under malt barley following fallow and pea than following malt barley in July 2010. Similarly, N_2O flux was greater under malt barley following pea than following malt barley and fallow in May and June 2011. Total N_2O flux from March to November was greater under fallow with 0 kg N ha^{-1} than under fallow with 80 kg N ha^{-1} and under malt barley and pea with 0 kg N ha^{-1} in 2011 Phase I (Table 4). Averaged across N fertilization, total N_2O flux was greater under fallow than under malt barley in Phase I and greater under malt barley following pea than following malt barley and fallow in Phase II in 2011. Averaged across cropping sequences, total N_2O flux was greater with 80 than with 0 kg N ha^{-1} in 2010 Phase I and in 2009 and 2011 Phase II.

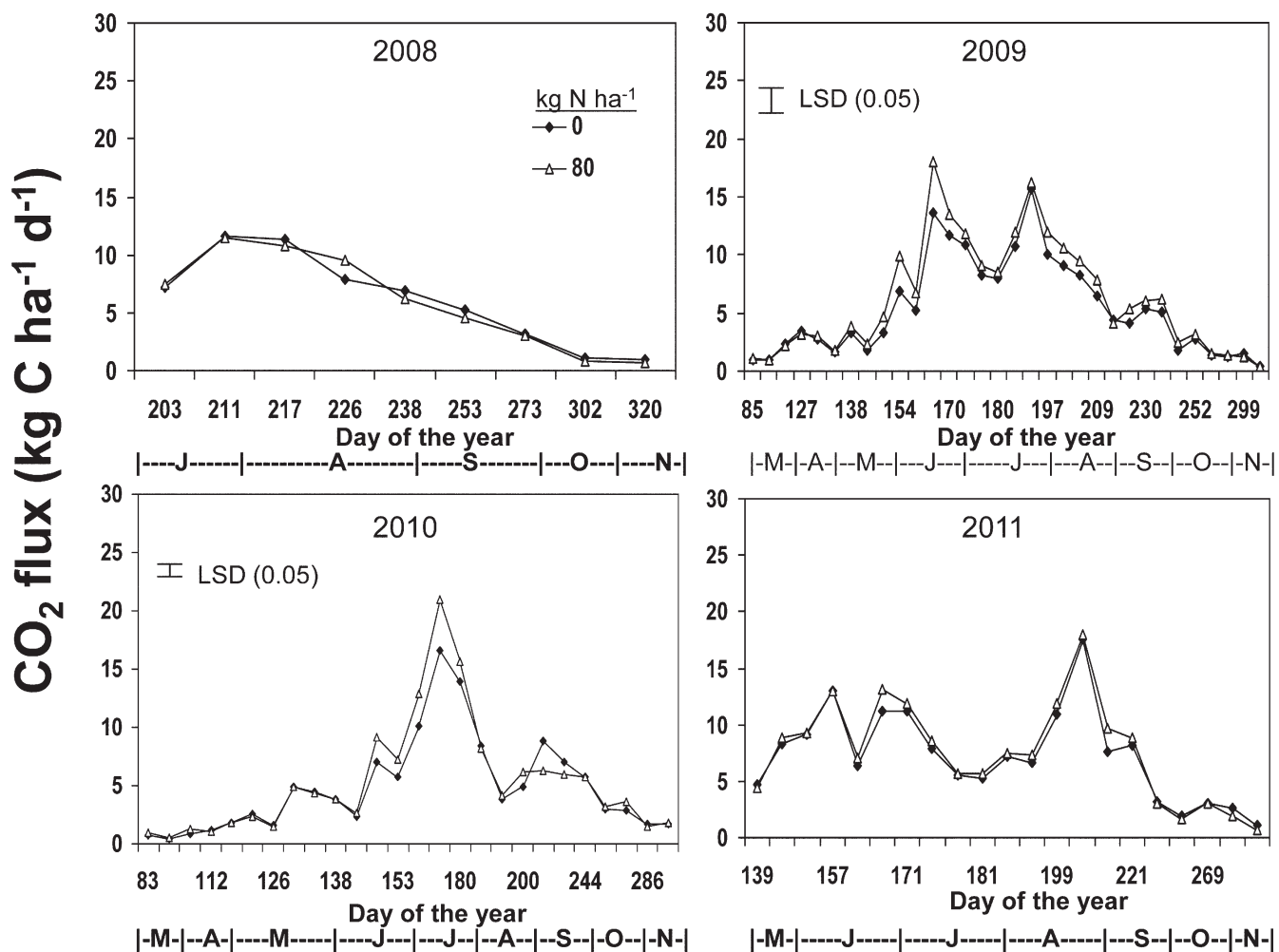


Fig. 5. Effect of N fertilization on soil surface CO_2 flux from March to November 2008 to 2011. Uppercase letter at the bottom of the figure denotes month of the year.

While greater N_2O flux with N fertilization than without in Phases I and II has been known to be a result of increased N sub-

strate availability as described above, greater fluxes under pea and fallow than under malt barley in Phase I or increased fluxes under

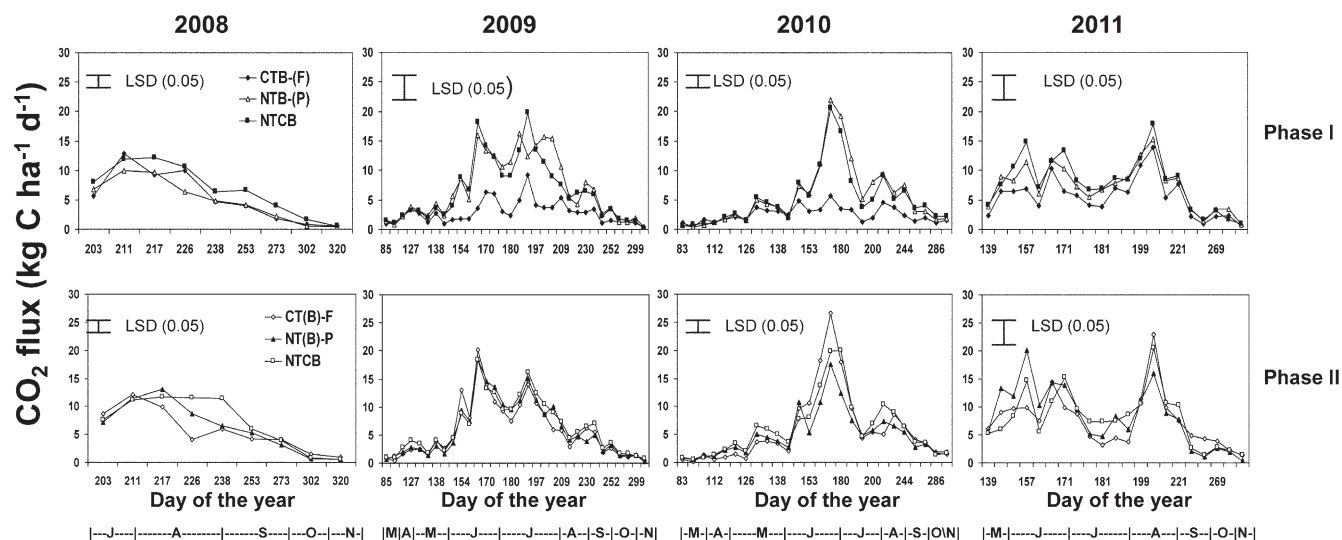


Fig. 6. Effect of cropping sequence phase on soil surface CO_2 flux from March to November 2008 to 2011. CTB-F denotes conventional-tilled malt barley-fallow; NTB-P, no-tilled malt barley-pea; and NTCB, no-tilled continuous malt barley. The letter in the parenthesis in the cropping sequence denotes a particular crop in each phase (B, malt barley; F, fallow; and P, pea). Uppercase letter at the bottom of the figure denotes month of the year.

malt barley following pea and fallow compared to following malt barley in Phase II were likely due to increased soil $\text{NO}_3\text{-N}$ and/or water content. Pea, being a legume, fixes N from the atmosphere and can enrich soil $\text{NO}_3\text{-N}$ after the residue is returned to the soil (Sainju, 2008; Sainju et al., 2011). Soil water uptake is lower for pea than for spring wheat, thereby resulting in more water available for succeeding crops (Lenssen et al., 2007). Fallowing results in greater soil water and $\text{NO}_3\text{-N}$ contents due to absence of crops during fallow and increased organic matter mineralization as a result of enhanced microbial activity from increased soil temperature and water content (Haas et al., 1974; Aase and Pikul, 1995; Sainju, 2008). Several researchers (Aulakh et al., 1982; Lemke et al., 1999; Dusenbury et al., 2008) have also noted increased N_2O flux under pea and fallow compared to spring wheat in western Montana and Alberta.

Methane

Methane flux varied with N fertilization in 2008 and 2010 and with date of sampling in all years (Table 5). Although cropping sequence had no effect on CH_4 flux, it interacted significantly with N fertilization in 2009 and 2011 and with date of sampling in all years. Nitrogen fertilization, date of sampling, and cropping sequence \times N fertilization and cropping sequence \times date of sampling interactions were significant for CH_4 flux for cropping phases in various years.

Methane flux was negative on most sampling dates, resulting in uptake by the soil (Fig. 9). Aerobic dryland soils act as sink for CH_4 due to its consumption by methanotrophs (Sylvia et al., 1998) and CH_4 uptake can be higher as soils further dry up (Liebig et al., 2010). In 2008, CH_4 flux increased from $-3 \text{ g C ha}^{-1} \text{ d}^{-1}$ in July to $10 \text{ g C ha}^{-1} \text{ d}^{-1}$ in August and then declined to $-8 \text{ g C ha}^{-1} \text{ d}^{-1}$ in September. In other years, CH_4 flux varied between -7 to $5 \text{ g C ha}^{-1} \text{ d}^{-1}$. The CH_4 flux values of -8 to $10 \text{ g C ha}^{-1} \text{ d}^{-1}$ obtained in this experiment were within or greater than the ranges of -12 to $5 \text{ g C ha}^{-1} \text{ d}^{-1}$ under dryland spring wheat–fallow and fallow systems in western Nebraska and central North Dakota (Kessavalou et al., 1998; Liebig et al., 2010).

In 2008, CH_4 uptake was greater in CTB–F than in NTCB in August and October but was greater in NTCB and NTB–P than in CTB–F in September (Fig. 9). In 2009, CH_4 uptake was greater in CTB–F in April, June, and October but was greater in NTB–P and NTCB in August and September. In 2010, CH_4 uptake was greater in NTB–P than in other cropping sequences in May, August, and September but was greater

Table 3. Effects of cropping sequence and N fertilization on average (total from March to November in each year) soil surface greenhouse gas fluxes from 2008 to 2011.

Cropping sequence†	N fertilization	Year	CO_2 flux	N_2O flux	CH_4 flux
	kg N ha ⁻¹		Mg C ha ⁻¹	g N ha ⁻¹	g C ha ⁻¹
CTB–F	0		1.00	327	–347
	80		1.02	302	–263
NTB–P	0		1.16	312	–369
	80		1.30	378	–240
NTCB	0		1.29	285	–223
	80		1.36	299	–370
LSD (0.05)			ns‡	ns	142
Means					
CTB–F			1.01b§	316a	–306a
NTB–P			1.23a	348a	–304a
NTCB			1.32a	291a	–295a
	0		1.15b	308a	–314a
	80		1.23a	329a	–291a
		2008	0.80c	315b	–222c
		2009	1.38a	227c	–625a
		2010	1.17b	188c	–296c
		2011	1.30ab	391a	–410b
Significance					
Cropping sequence (C)			**	ns	ns
N fertilization (F)			*	ns	ns
C \times F			ns	ns	**
Year (Y)			***	***	***
C \times Y			*	**	ns
F \times Y			ns	ns	*
C \times F \times Y			*	*	ns

* Significant at $P = 0.05$.

** Significant at $P = 0.01$.

*** Significant at $P = 0.001$.

† Cropping sequences are CTB–F, conventional-tilled malt barley–fallow; NTB–P, no-tilled malt barley–pea; and NTCB, no-tilled continuous malt barley.

‡ ns, not significant.

§ Numbers followed by different letters in a column within a set are significantly different at $P \leq 0.05$ by the least square means test.

in NTCB and CTB–F in July. In 2011, CH_4 uptake was also greater in NTB–P in May and June but was greater in NTCB and CTB–F in August. Total CH_4 uptake from March to November was greater in NTCB with 80 kg N ha^{-1} and NTB–P with 0 kg N ha^{-1} than in NTCB with 0 kg N ha^{-1} in 2009 and 2011 (Table 5). Averaged across cropping sequences, total CH_4 uptake was greater with 0 than with 80 kg N ha^{-1} in 2008 but the trend reversed in 2010. Averaged across years, total CH_4 uptake was greater in NTCB with 80 kg N ha^{-1} and NTB–P with 0 kg N ha^{-1} than in NTCB with 0 kg N ha^{-1} (Table 3). Averaged across treatments, total CH_4 uptake was greater in 2009 than in other years.

In contrast to CO_2 and N_2O fluxes, CH_4 uptake varied with cropping sequence and N fertilization at various sampling dates and years. The trend of CH_4 uptake for treatments with sampling dates did not appear to be related with trends in soil temperature or water content. Greater CH_4 uptake in NTCB with 80 kg N ha^{-1} and in NTB–P with 0 kg N ha^{-1} , however, suggests that greater root growth due to increased N supply by N fertilizer or pea residue probably stimulated the activity of meth-

Table 4. Effects of cropping sequence and N fertilization on total soil surface N₂O flux from March to November 2008 to 2011.

Cropping sequence†	N fertilization	Total N ₂ O flux‡											
		2008			2009			2010			2011		
		Phase I	Phase II	Mean	Phase I	Phase II	Mean	Phase I	Phase II	Mean	Phase I	Phase II	Mean
	kg N ha ⁻¹	g N ha ⁻¹											
CTB-F	0	281	277	279	243	205	224	182	203	193	704	246	475
	80	331	317	324	253	245	249	217	164	191	324	282	303
NTB-P	0	300	274	287	229	231	230	182	134	158	320	547	434
	80	371	317	344	205	238	222	238	194	216	497	637	567
NTCB	0	365	342	354	175	227	201	178	176	175	190	285	238
	80	314	293	304	224	250	237	213	169	191	343	317	330
LSD (0.05)		ns§	ns	66	ns	ns	ns	ns	ns	ns	362	ns	171
Means													
CTB-F		307a¶	297a	302a	248a	227a	238a	201a	182a	192a	514a	236b	375ab
NTB-P		335a	296a	316a	217a	236a	227a	210a	164a	187a	410ab	592a	501a
NTCB		339a	317a	328a	201a	238a	220a	194a	171a	183a	266b	301b	284b
	0	315a	297a	306a	217a	219b	218a	180b	171a	176b	405a	358b	382a
	80	339a	309a	324a	227a	245a	236a	222a	176a	199a	388a	412a	400a
Significance													
Cropping sequence (C)		ns	ns	ns	ns	ns	ns	ns	ns	ns	*	*	*
N fertilization (F)		ns	ns	ns	ns	*	ns	**	ns	*	ns	*	ns
C × F		ns	ns	*	ns	ns	ns	ns	ns	ns	*	ns	*
Date of sampling (D)		***	***	***	***	***	***	***	***	***	***	***	***
C × D		*	ns	ns	*	ns	*	ns	*	*	**	***	***
F × D		ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
C × F × D		ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns

* Significant at $P = 0.05$.** Significant at $P = 0.01$.*** Significant at $P = 0.001$.

† Cropping sequences are CTB-F, conventional-tilled malt barley-fallow; NTB-P, no-tilled malt barley-pea; and NTCB, no-tilled continuous malt barley.

‡ Phase I of the cropping sequence includes fallow in CTB-F, pea in NTB-P, and malt barley in NTCB and Phase II includes malt barley in all cropping sequences.

§ ns, not significant.

¶ Numbers followed by different letters in a column within a set are significantly different at $P \leq 0.05$ by the least square means test.

anotrophs that absorb CH₄. When N was jointly supplied by N fertilizer and pea residue, such as in NTB-P with 80 kg N ha⁻¹, CH₄ uptake was probably reduced because of excess level of soil inorganic N. Reduced root growth due to lower level of soil inorganic N as a result of absence of N fertilization also probably reduced the activity of methanotrophs, thereby resulting in lower CH₄ uptake in NTCB with 0 kg N ha⁻¹. Several researchers (Bronson and Mosier, 1994; Powlson et al., 1997) have reported that N fertilization reduced soil CH₄ uptake compared to no N fertilization while others (Amos et al., 2005; Mosier et al., 2006) found no effect of N fertilization on the uptake. Since GHG measurements were taken from July to November in 2008 when precipitation was minimal (Fig. 3), excluding 2008, greater CH₄ uptake in 2009 than in 2010 and 2011, however may be a result of drier soil conditions (Table 1), a case similar to that reported by Liebig et al. (2010).

Among crop species, CH₄ uptake also varied at various measurement dates (Fig. 10). In 2008, CH₄ uptake was greater under fallow in July but was greater under malt barley in August and September in Phase I. In 2009, CH₄ uptake was similarly greater under fallow in April and May but was greater under malt barley and pea in June. In Phase II, CH₄ uptake varied under malt

barley following malt barley, pea, or fallow at various measurement dates from 2008 to 2011. Total CH₄ uptake from March to November was greater under pea with 0 kg N ha⁻¹ than under fallow with 80 kg N ha⁻¹ in 2011 Phase I (Table 5). Total CH₄ uptake was greater with 80 than with 0 kg N ha⁻¹ under malt barley following malt barley in 2009 Phase II. Similarly, total CH₄ uptake was greater under malt barley following fallow with 0 kg N ha⁻¹ and following malt barley with 80 kg N ha⁻¹ than under malt barley following pea with 80 kg N ha⁻¹ or following malt barley with 0 kg N ha⁻¹ in 2011 Phase II. Averaged across crop species, total CH₄ uptake was greater with 80 than with 0 kg N ha⁻¹ in 2010 Phase I and 2009 Phase II but was greater with 0 than with 80 kg N ha⁻¹ in 2008 Phase II. Unlike CO₂ and N₂O fluxes, variability of crop species with N fertilization at various measurement dates and years on CH₄ fluxes suggests that these treatments interacted variably on CH₄ emissions under dryland cropping systems.

Management Implications

For identifying a management practice that can mitigate GHG emissions during a crop growing season (summer and fall), CO₂ equivalents of total N₂O and CH₄ fluxes from March

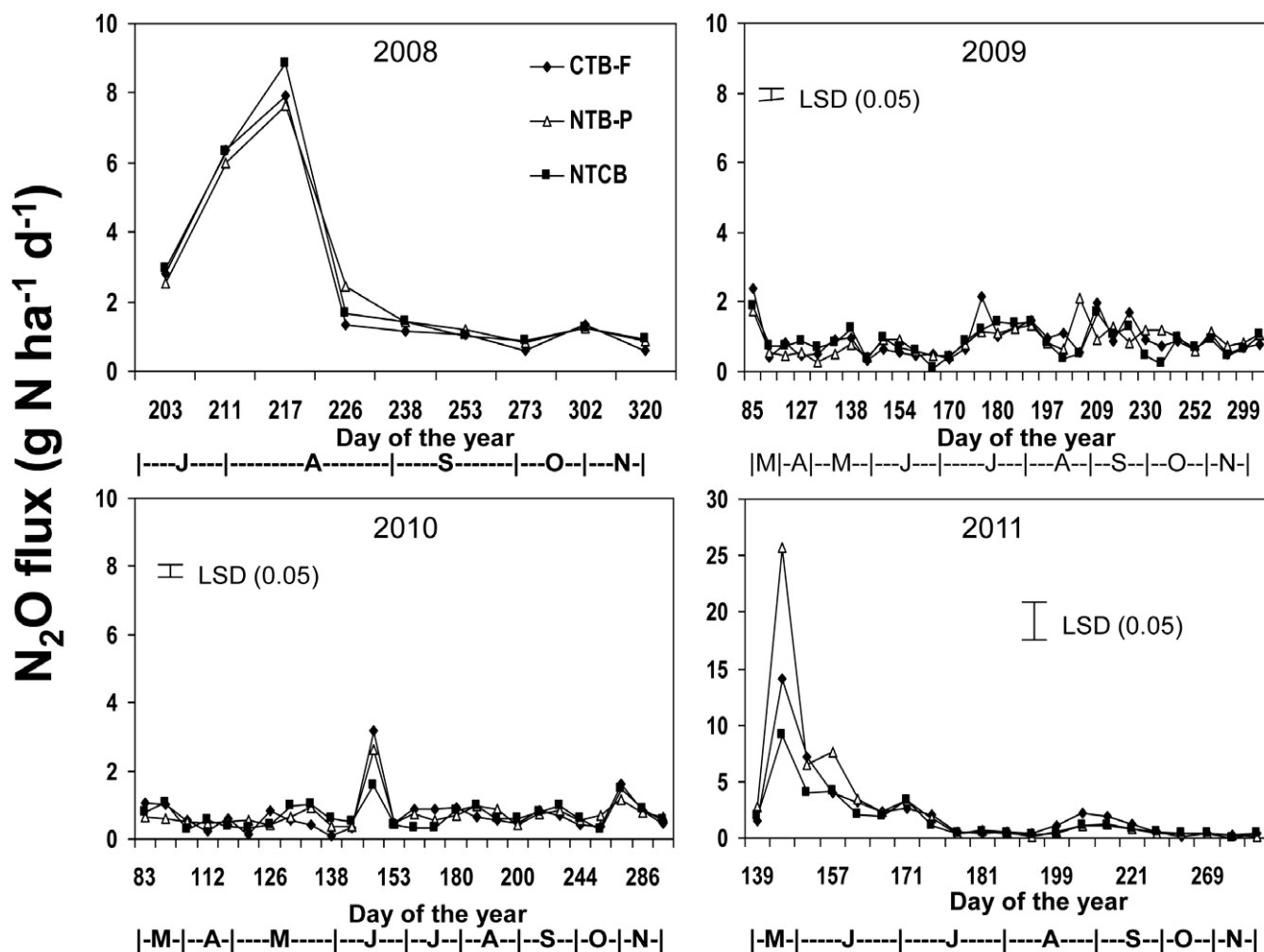


Fig. 7. Effect of cropping sequence on soil surface N_2O flux from March to November 2008 to 2011. CTB-F denotes conventional-tilled malt barley-fallow; NTB-P, no-tilled malt barley-pea; and NTCB, no-tilled continuous malt barley. Note the change in y axis scale in 2011 compared to other years. Uppercase letter at the bottom of the figure denotes month of the year.

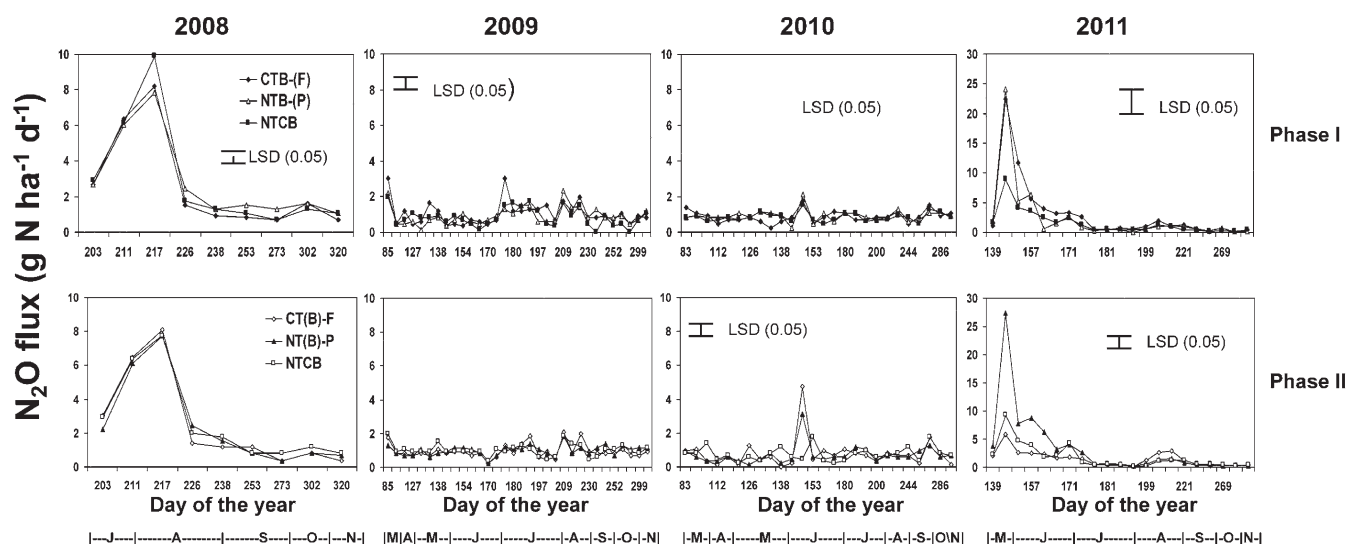


Fig. 8. Effect of cropping sequence phase on soil surface N_2O flux from March to November 2008 to 2011. CTB-F denotes conventional-tilled malt barley-fallow; NTB-P, no-tilled malt barley-pea; and NTCB, no-tilled continuous malt barley. The letter in the parenthesis in the cropping sequence denotes a particular crop in each phase (B, malt barley; F, fallow; and P, pea). Note the changes in y axis scale in 2011 Phases I and II compared to other years. Uppercase letter at the bottom of the figure denotes month of the year.

Table 5. Effects of cropping sequence and N fertilization on total soil surface CH₄ flux from March to November 2008 to 2011.

Cropping sequence†	N fertilization	Total CH ₄ flux‡											
		2008			2009			2010			2011		
		Phase I	Phase II	Mean	Phase I	Phase II	Mean	Phase I	Phase II	Mean	Phase I	Phase II	Mean
	kg N ha ⁻¹	g C ha ⁻¹											
CTB-F	0	-45	-675	-360	-717	-543	-630	-375	-172	-274	-373	-583	-478
	80	-224	-78	-151	-586	-642	-614	-363	-148	-256	-241	-361	-301
NTB-P	0	-222	-493	-376	-693	-689	-691	-229	-314	-272	-654	-422	-538
	80	71	80	76	-669	-525	-597	-401	-340	-371	-472	-139	-306
NTCB	0	-371	-186	-279	-720	-120	-420	-50	-293	-172	-300	-231	-266
	80	-316	-205	-261	-689	-911	-800	-451	-413	-432	-552	-581	-566
LSD (0.05)		ns§	ns	ns	ns	422	271	ns	ns	ns	411	317	182
Means	0	-212a¶	-451b	-332b	-717a	-451a	-581a	-217b	-260a	-239a	-441a	-413a	-427a
	80	-156a	-68a	-112a	-645a	-691b	-668a	-406a	-300a	-353b	-422a	-361a	-392a
Significance													
Cropping sequence (C)		ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
N fertilization (F)		ns	***	*	ns	***	ns	*	ns	*	ns	ns	ns
C × F		ns	ns	ns	ns	***	*	ns	ns	ns	*	**	***
Date of sampling (D)		***	***	***	***	***	***	***	***	***	***	**	***
C × D		*	*	*	*	*	*	ns	*	*	ns	*	*
F × D		ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
C × F × D		ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns

* Significant at $P = 0.05$.** Significant at $P = 0.01$.*** Significant at $P = 0.001$.

† Cropping sequences are CTB-F, conventional-tilled malt barley-fallow; NTB-P, no-tilled malt barley-pea; and NTCB, no-tilled continuous malt barley.

‡ Phase I of the cropping sequence includes fallow in CTB-F, pea in NTB-P, and malt barley in NTCB and Phase II includes malt barley in all cropping sequences.

§ ns, not significant.

¶ Numbers followed by different letters in a column within a set are significantly different at $P \leq 0.05$ by the least square means test.

to November were calculated by considering that N₂O and CH₄ were 298 and 25 times, respectively, more powerful than CO₂ in terms of global warming potential. These values were then added to total CO₂ flux from March to November. Total CO₂ equivalents of GHGs, averaged across years, amounted to 1.27, 1.28, 1.42, 1.63, 1.54, 1.61 Mg CO₂-C ha⁻¹ for CTB-F with 0 kg N ha⁻¹, CTB-F with 80 kg N ha⁻¹, NTB-P with 0 kg N ha⁻¹, NTB-P with 80 kg N ha⁻¹, NTCB with 0 kg N ha⁻¹, and NTCB with 80 kg N ha⁻¹, respectively. Although CTB-F with 0 and 80 kg N ha⁻¹ produced lower CO₂ equivalents of GHGs than other management practices, fallowing in CTB-F reduces annualized crop yield and soil organic matter (Lenssen et al., 2007; Sainju, 2008; Sainju et al., 2009) and becomes unsustainable and uneconomical (Aase and Schaefer, 1996). Because of the intermediate level of CO₂ equivalent of GHGs, NTB-P with 0 kg N ha⁻¹ might be used as a management option to mitigate GHG emissions under dryland cropping systems. Although pea residue adds about 20 kg N ha⁻¹, 40 kg N ha⁻¹ has been found to produce greater malt barley grain and biomass yields than 0 kg N ha⁻¹ but similar to 80 and 120 kg N ha⁻¹ in NTB-P (Sainju, 2008). Therefore, NTB-P with 0 kg N ha⁻¹ may mitigate GHG emissions but may not sustain malt barley yields. Further studies are underway to examine if NTB-P with reduced N fertilization rate might mitigate GHG emissions and sustain crop yields. Other benefits of using crop rotation com-

pared to monocropping include reduced infestation of weeds, diseases, and pests. For evaluating global warming potential of management systems, however, soil C dynamics (which replaces CO₂ flux) and CO₂ emissions associated with crop production inputs and machinery use, concurrently with CO₂ equivalence of N₂O and CH₄ emissions, need to be considered.

CONCLUSIONS

Differences in tillage, cropping sequence, crop species, and N fertilization rates among treatments resulted in different GHG fluxes at various measurement dates and years. While CO₂ and N₂O fluxes peaked immediately following substantial precipitation events and/or N fertilization during increased soil temperature and water content, CH₄ flux varied with treatments and measurement dates. Carbon dioxide flux was greater in no-tilled continuous cropping than in conventional-tilled crop-fallow and with N fertilization than without. In contrast, CH₄ uptake was greater in NTCB with 80 kg N ha⁻¹ and NTB-P with 0 kg N ha⁻¹ than in NTCB with 0 kg N ha⁻¹. Carbon dioxide flux was greater under malt barley than under pea or fallow but N₂O flux was greater under pea and fallow than under malt barley. Although CTB-F with or without N fertilization had lower CO₂ equivalents of GHG emissions, NTB-P without N fertilization may be used as a management option to mitigate GHG emissions in the dryland cropping systems in eastern Montana

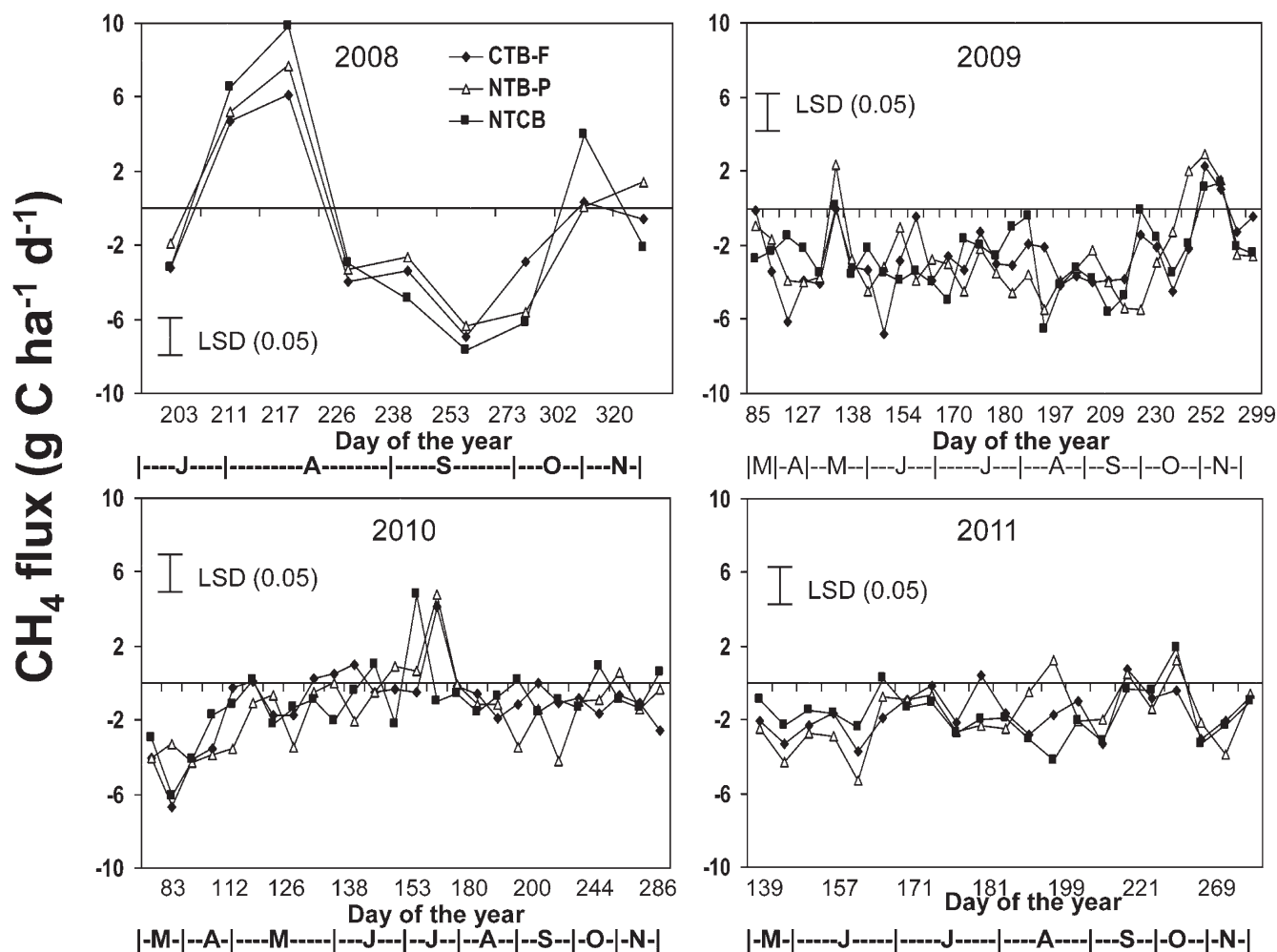


Fig. 9. Effect of cropping sequence on soil surface CH_4 flux from March to November 2008 to 2011. CTB-F denotes conventional-tilled malt barley-fallow; NTB-P, no-tilled malt barley-pea; and NTCB, no-tilled continuous malt barley. Uppercase letter at the bottom of the figure denotes month of the year.

because of its intermediate GHG level and known slightly favorable effect on malt barley yield. Further studies are underway to

evaluate if NTB-P with reduced rate of N fertilization can mitigate GHG emissions and sustain malt barley yields compared to

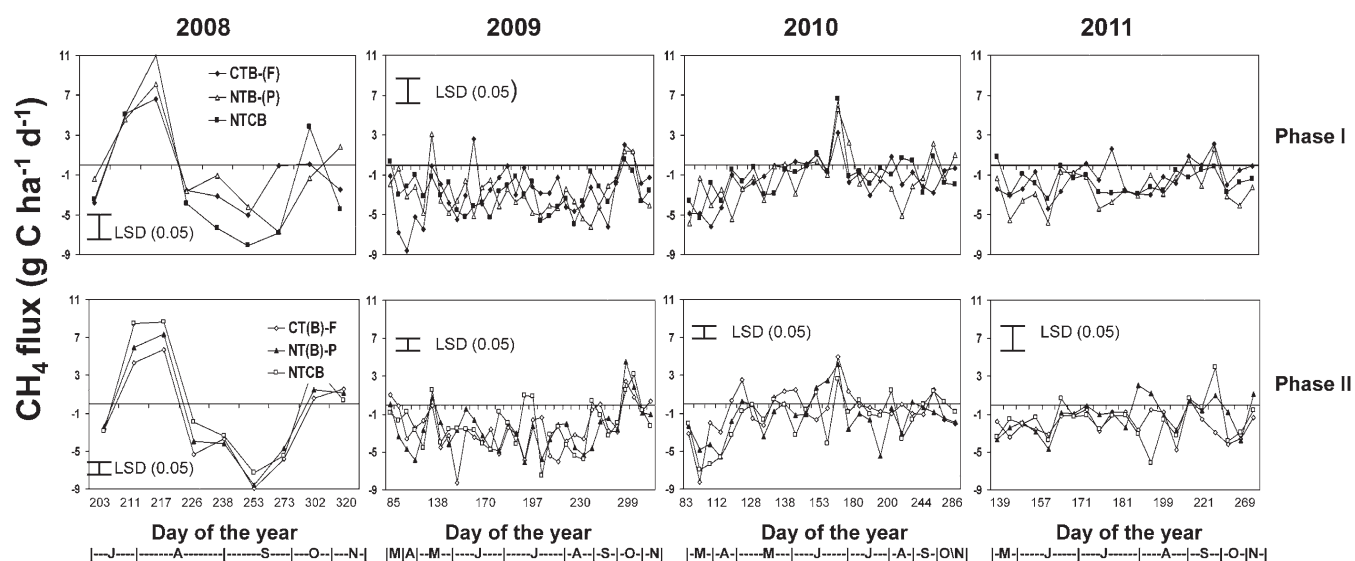


Fig. 10. Effect of cropping sequence phase on soil surface CH_4 flux from March to November 2008 to 2011. CTB-F denotes conventional-tilled malt barley-fallow; NTB-P, no-tilled malt barley-pea; and NTCB, no-tilled continuous malt barley. The letter in the parenthesis in the cropping sequence denotes a particular crop in each phase (B, malt barley; F, fallow; and P, pea).

other treatments. Additional information on soil C dynamics and CO₂ contributions from production inputs and machine operations, however, are needed to account for global warming potentials of management practices.

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